

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1684.26 Seconds
(without alignments)
7460.491 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacaat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
	1	344.2	66.6	796	14	CB959991	CB959991 AGENCOURT
c	2	331.6	64.1	558	9	AI503976	AI503976 vm43d08.x
c	3	330.6	63.9	673	12	BM984670	BM984670 UI-CF-EC1
c	4	329.8	63.8	623	9	AW146128	AW146128 um37e10.x
c	5	326.6	63.2	575	9	AI248089	AI248089 qh69f05.x
c	6	316.6	61.2	549	9	AI169253	AI169253 EST215088
c	7	315.8	61.1	558	9	AI265629	AI265629 uj04b07.x
c	8	314.8	60.9	498	9	AA542914	AA542914 ni98c10.s
	9	310	60.0	614	14	CD373004	CD373004 UI-R-GR0-
	10	309	59.8	816	9	AI119218	AI119218 ue94h02.y
	11	303.6	58.7	594	10	BF383724	BF383724 602044632
c	12	299.8	58.0	527	9	AA913900	AA913900 ol35g05.s
c	13	289.6	56.0	642	9	AI876493	AI876493 uj59b10.x
c	14	287.4	55.6	499	9	AW495481	AW495481 UI-M-BH3-
c	15	276	53.4	468	9	AI169770	AI169770 EST215669
	16	274.4	53.1	882	9	AI604642	AI604642 vm43d08.y
c	17	268.2	51.9	430	9	AI478804	AI478804 tm52e04.x
c	18	263.2	50.9	653	13	BQ200567	BQ200567 UI-R-DZ1-
	19	258.4	50.0	608	9	AL599807	AL599807 DKFzp3130
c	20	254.6	49.2	486	9	AA993659	AA993659 ot85g11.s
c	21	254.2	49.2	521	9	AW493459	AW493459 UI-M-BH3-
	22	254.2	49.2	559	12	BI715603	BI715603 ic34h10.y
	23	254.2	49.2	602	13	BU590710	BU590710 AGENCOURT
	24	254.2	49.2	621	12	BI221656	BI221656 602936980
	25	254.2	49.2	1658	11	AK081019	AK081019 Mus muscu
	26	254	49.1	356	9	AW297586	AW297586 UI-H-BW0-
c	27	253.2	49.0	595	9	AI573421	AI573421 mo04b11.x
c	28	252.6	48.9	499	12	BI676839	BI676839 ic56a08.x
c	29	252.6	48.9	500	9	AA945553	AA945553 EST201052
c	30	252.6	48.9	525	9	AA963258	AA963258 UI-R-El-g
	31	251.4	48.6	482	9	AA456717	AA456717 aa13h06.r
c	32	251	48.5	706	9	AI401719	AI401719 th30b10.x
c	33	249.4	48.2	525	9	AI599751	AI599751 EST251454
	34	248.6	48.1	665	9	AA690767	AA690767 vu57d12.r
	35	247.8	47.9	559	12	BI715465	BI715465 ic33b09.y
	36	247.4	47.9	799	9	AI314558	AI314558 uj48d07.y
c	37	247.2	47.8	499	12	BI294072	BI294072 UI-R-DK0-
c	38	244.2	47.2	502	9	AI104669	AI104669 EST213958
c	39	243	47.0	561	12	BI714874	BI714874 ic33b09.x
c	40	240.6	46.5	564	12	BI714981	BI714981 ic34h10.x
	41	239.2	46.3	2170	11	AK038119	AK038119 Mus muscu
	42	237.4	45.9	558	12	BI715475	BI715475 ic33c08.y
c	43	237.2	45.9	480	9	AA621551	AA621551 af47c10.s
	44	236.8	45.8	512	9	AI876203	AI876203 uj59b10.y
	45	234.2	45.3	949	14	CB589117	CB589117 AGENCOURT

ALIGNMENTS

RESULT 1
 CB959991
 LOCUS CB959991 796 bp mRNA linear EST 29-APR-2003
 DEFINITION AGENCOURT_13888044 NIH_MGC_147 Homo sapiens cDNA clone
 IMAGE:30341081 5', mRNA sequence.
 ACCESSION CB959991
 VERSION CB959991.1 GI:30216107
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 796)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM371 row: p column: 18
 High quality sequence stop: 707.
 FEATURES Location/Qualifiers
 source 1. 796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30341081"
 /tissue_type="Human Placenta"
 /lab_host="DH10B TonA"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 allI-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."
 BASE COUNT 224 a 197 c 191 g 184 t
 ORIGIN
 Query Match 66.6%; Score 344.2; DB 14; Length 796;
 Best Local Similarity 87.3%; Pred. No. 8.3e-81;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 239

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 240 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 299

Qy 121 ACAGGCATCGTGGATGAGTGCCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 300 ACAGGCATCGTGGATGAGTGCCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 419

Qy 241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 ||||||||||||||||
 Db 420 ATGCCCCAAGACCCAG----- 434

Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Db 435 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 490

Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
 ||||| |||||||| |||||||||||||||| |||| |||||||||||| ||||||||
 Db 491 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 550

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
 ||||| |||||||| ||||| |||||| ||| |||||||||||||||| |||||||
 Db 551 TGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 610

Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 |||||| ||| ||||||||||||||||||||||||||||||||
 Db 611 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 651

RESULT 2

AI503976/c

LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999

DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI503976

VERSION AI503976.1 GI:4401827

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Qy 298 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCGAGGAAAACAAGAACTA 357
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 230 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGAAAGTGCGAGGAAAACAAGACCTA 171

Qy 358 CAGGATGTGA-GAAGACCCTTCTGAGGAGTGAAGAAGGCACAGGCCACCGCAGGACCCTTTG 416
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 CAGAATGTAGGAGGAGCCTCCCAACGAGCAGAAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 470
 | | | | | | | | | | | | | | | | | | | | | | | |
Db 110 CTGCTTGAGCAACCTGCAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 51

Qy 471 ACATTTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTA AACAT 517
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTA AACAT 3

FEATURES	Location/Qualifiers
source	1..673 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

/clone="UI-CF-EC1-abj-k-24-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_LIB=UI-CF-EC1
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_SEQ=AAGTGCTTAC"

BASE COUNT 152 a 164 c 169 g 188 t
ORIGIN

Query Match 63.9%; Score 330.6; DB 12; Length 673;
Best Local Similarity 86.9%; Pred. No. 3.3e-77;
Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;

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Qy            1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy            61  AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
   ||||| ||||||||| |||||||||||||||||||||||||||||||||||||||
Db            432 AGGGG-TTTTATTTTCAGCAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy            121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy            181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 254

Qy            241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
   |||||||||||||
Db            253 ATGCCCAAGACCCAG----- 239

Qy            301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
   ||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db            238 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 183

Qy            361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
   ||||| ||||||||| ||||||||||||| |||| ||||||||||||| |||||||
```

Db 182 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 123

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTC 477
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Db 122 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 63

Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 62 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 22

RESULT 4

AW146128/c

LOCUS AW146128 623 bp mRNA linear EST 10-OCT-2000

DEFINITION um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AW146128

VERSION AW146128.1 GI:6167864

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 623)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1006958

Seq primer: custom primer used

High quality sequence stop: 499.

FEATURES

source

Location/Qualifiers

1. .623

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:2247498"

/dev_stage="embryo, 14 dpc"

/lab_host="DH10B"

/clone_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);

Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 123 a 138 c 170 g 191 t 1 others
ORIGIN

Query Match 63.8%; Score 329.8; DB 9; Length 623;
Best Local Similarity 80.6%; Pred. No. 5.3e-77;
Matches 425; Conservative 0; Mismatches 92; Indels 10; Gaps 3;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      541 GGACCAGAGACCCTTTTCGGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 482

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGGCACCTCAG 422

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     421 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAAATGTAC 362

Qy     181 TGGCGACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        || || || || ||||| | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     361 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 302

Qy     241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
        ||||| ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db     301 ATGCCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 242

Qy     298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
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Db     241 AGAAGGAAAGGAAGTACATTTGAAGAACCCAAGTAGAGGAAGTGCAGGAAACAAGACCTA 182

Qy     358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 416
        ||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     181 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 122

Qy     417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 470
        ||      | ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTACCAAATAACAATAATAAGTCCAATA 62

Qy     471 ACATTTCAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
        ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 ACATTACAAAGATGGGCATTTCCTCCCAATGAAATATACAAGTAAACAT 15

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RESULT 5

AI248089/c

LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998

DEFINITION qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA

clone IMAGE:1849953 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI248089

VERSION AI248089.1 GI:3843486

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 575)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 918 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 380.

FEATURES

source Location/Qualifiers

1. .575
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1849953"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 135 a 152 c 131 g 156 t 1 others

ORIGIN

Query Match 63.2%; Score 326.6; DB 9; Length 575;
Best Local Similarity 86.6%; Pred. No. 3.7e-76;
Matches 438; Conservative 0; Mismatches 15; Indels 53; Gaps 5;

Qy 16 TGC GGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75
|||||

Db 551 TGC GGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTTC 492
|||||

Qy 76 AAC AAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT 135
|||||

Db 491 AAC AAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT 432
|||||

Qy 136 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 195
 |||
 Db 431 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 372
 Qy 196 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGACATGCCCAAGACCCAG 255
 |||
 Db 371 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGACATGCCCAAGACCCAG 312
 Qy 256 AAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGAAGGAAAGGAAGTACA 315
 |||
 Db 311 -----AAGGAAGTACA 301
 Qy 316 TTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTA-GAAGACCC 374
 |||
 Db 300 TTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCC 241
 Qy 375 TTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCAC-AGTTACCTG 433
 | |||
 Db 240 TCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTACCTG 181
 Qy 434 -TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCATTTTC 491
 |||| |||| ||| |||
 Db 180 TTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTAAAGATGGGCGTTTC 121
 Qy 492 CCCCAATGAAATACACAAGTAAACAT 517
 |||
 Db 120 CCCCAATGAAATACACAAGTAAACAT 95

RESULT 6

AI169253/c

LOCUS AI169253 549 bp mRNA linear EST 08-JAN-1999
 DEFINITION EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
 RKIBP33 3' end, mRNA sequence.

ACCESSION AI169253

VERSION AI169253.1 GI:4134375

KEYWORDS EST.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 549)

AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Kerlavage,A.R. and Adams,M.D.

TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
 Gene Index

JOURNAL Unpublished

COMMENT On Oct 6, 1998 this sequence version replaced gi:3705561.

Other_ESTs: TC50779

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0208

Email: nhlee@tigr.org

Seq primer: M13-21.

FEATURES Location/Qualifiers
 source 1. .549
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="taxon:10118"
 /clone="RKIBP33"
 /clone_lib="Normalized rat kidney, Bento Soares"
 /note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI"
 BASE COUNT 112 a 140 c 133 g 164 t
 ORIGIN

Query Match 61.2%; Score 316.6; DB 9; Length 549;
 Best Local Similarity 80.8%; Pred. No. 1.7e-73;
 Matches 421; Conservative 0; Mismatches 89; Indels 11; Gaps 4;

```

Qy      8 AGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67
      |||| || |||||||||||||||||||| ||||| ||| ||||||||| |||||
Db      549 AGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCAAGGGGCT 490

Qy      68 TTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCA 127
      |||| |||||||||||||||||| ||||||||||| ||| ||||| || ||||| |||
Db      489 TTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCGAAGGGCACCACAGACGGGCA 430

Qy      128 TCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCAC 187
      | ||||||||| ||||||||||||||| ||||||||||||| ||||| || |||
Db      429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy      188 CCCTCAAGCCTGCCAAGTCAGCTCGTCTGTCCGTGCCCAGCGCCACACCGACATGCCCA 247
      | || ||||| | ||||||||| || |||| ||||||||||||| |||||||||
Db      369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy      248 AGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---GAGAAGGA 304
      |||| ||||| ||||| ||| || ||||| | |||| || |||||
Db      309 AGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy      305 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 364
      ||||||||| |||||||||||||||| ||||||||||||| ||||| |||
Db      249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy      365 TA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 423
      || || || || ||||| || || || || ||||| || |||||
Db      189 TAGGAGGAGCCTCCCAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy      424 CAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCACATTTTC 477
      | ||||| |||| ||| |||| || |||| |||| || |||||
Db      129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTTC 70

Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
      | |||| ||||||||| |||||||||||||||||||
Db      69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 29

```

RESULT 7
 AI265629/c
 LOCUS AI265629 558 bp mRNA linear EST 18-NOV-1998
 DEFINITION uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone

IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI265629

VERSION AI265629.1 GI:3883787

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished

COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:975225
Seq primer: custom primer used
High quality sequence stop: 495.

FEATURES
source Location/Qualifiers
1. .558
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890901"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 106 a 135 c 156 g 161 t

ORIGIN

Query Match 61.1%; Score 315.8; DB 9; Length 558;

Best Local Similarity 80.8%; Pred. No. 2.7e-73;
Matches 408; Conservative 0; Mismatches 87; Indels 10; Gaps 3;

```
Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      506 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 447

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      446 AGGGGCTTTTACTTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 387

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      386 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 327

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        || || || || ||||| || || ||||| ||||| ||||| ||||| |||||
Db      326 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267

Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
        ||||| ||||| ||||| || ||||| || ||||| ||||| ||||| ||
Db      266 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAAACAAGAAAACGAAGCTGCAAAGG 207

Qy      298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      206 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 147

Qy      358 CAGGATGTA-GAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 416
        ||| ||||| || || ||||| ||||| || || || ||||| ||||| |||||
Db      146 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCAGGATCCTTTG 87

Qy      417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 470
        || || ||||| || || ||||| || ||||| || ||||| || |||||
Db      86 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 27

Qy      471 ACATTTCAAAGATGGCATTTCCTCCC 495
        ||||| ||||| || |||||
Db      26 ACATTACAAAGATGGGCATTTCCTCCC 2
```

RESULT 8

AA542914/c

LOCUS AA542914 498 bp mRNA linear EST 19-AUG-1997

DEFINITION ni98c10.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984882 3'
similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION AA542914

VERSION AA542914.1 GI:2291394

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 498)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 603 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 412.

FEATURES Location/Qualifiers
source 1. .498
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:984882"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr21"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 105 a 135 c 123 g 135 t
ORIGIN

Query Match 60.9%; Score 314.8; DB 9; Length 498;
Best Local Similarity 86.2%; Pred. No. 4.9e-73;
Matches 450; Conservative 0; Mismatches 17; Indels 55; Gaps 7;

```

Qy      1 GGACCGGAGACGCTCTGCGGGGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59
          |||||
Db      476 GGACCGGAGAACTTTTGC GGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417

Qy      60 CAGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 119
          |||||
Db      416 CAGGGGC-TTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358

Qy      120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 179
          |||||
Db      357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298

Qy      180 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 239
          |||||
Db      297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238

Qy      240 CATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAG 299
          |||||

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Db      237 CATGCCCCAAGACCCAG----- 222
Qy      300 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 359
        ||||||||||||||||||| |||||||||||||||||||
Db      221 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 167
Qy      360 GGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 418
        ||||||| ||||||| ||||||| ||| ||||||| |||||||
Db      166 GGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCT 107
Qy      419 CTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
        |||||| |||||| ||| |||||| ||| |||||| |||||| ||||||
Db      106 CTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTT 47
Qy      477 CAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
        |||||| ||| |||||||||||||||||||||||
Db      46  AAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 5

```

RESULT 9

CD373004

LOCUS CD373004 614 bp mRNA linear EST 29-MAY-2003

DEFINITION UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 Rattus norvegicus cDNA clone
UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.

ACCESSION CD373004

VERSION CD373004.1 GI:31157094

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 614)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: James Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/rat.html>

Seq primer: M13 REVERSE.

FEATURES

source

Location/Qualifiers

1. .614

/organism="Rattus norvegicus"

/mol_type="mRNA"

Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
 || | |||| |||| || |||| | || ||| || |
 Db 536 CTGCTTGAGCAACCTGCANAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 595

Qy 477 CAA 479
 | |
 Db 596 CCA 598

RESULT 10

AI119218

LOCUS AI119218 816 bp mRNA linear EST 02-SEP-1998

DEFINITION ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI119218

VERSION AI119218.1 GI:3519542

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 816)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished

COMMENT Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:936407

Seq primer: custom primer used

High quality sequence stop: 473.

FEATURES

source

Location/Qualifiers

1. .816

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1498803"

/dev_stage="embryo, 14 dpc"

/lab_host="DH10B"

/clone_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);

Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTGGCCTACTGG], digested and cloned into distinct DraIII

BASE COUNT	230 a	219 c	172 g	187 t	8 others
ORIGIN					

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	323	GGACCAGAGACCCCTTTCGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG	382
Qy	61	AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	383	AGGGGCTTTTACTTTCACAAAGCCACAGGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG	442
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	443	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	502
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	240
Db	503	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC	562
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACCGAAGTCTCA---G	297
Db	563	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	622
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	623	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA	682
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	683	CAGAAATGTANGAGGAGCCTNCCACGGAGCAGAAATGCCACATCACCGCANGATCCTTTG	742
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATT	475
Db	743	CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT	801

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RESULT 11
BF383724
LOCUS      BF383724                594 bp    mRNA    linear    EST 27-NOV-2000
DEFINITION 602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5',
            mRNA sequence.
ACCESSION  BF383724
VERSION    BF383724.1  GI:11365029
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)

```

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9527 row: p column: 08
 High quality sequence stop: 589.

FEATURES Location/Qualifiers

source 1. .594
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4194295"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Li9"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t

ORIGIN

Query Match 58.7%; Score 303.6; DB 10; Length 594;
 Best Local Similarity 80.7%; Pred. No. 4.9e-70;
 Matches 394; Conservative 0; Mismatches 84; Indels 10; Gaps 3;

```

Qy      16 TGC GGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75
          |||
Db      107 TGC GGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC 166

Qy      76 AAC AAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT 135
          |||
Db      167 AAC AAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGAT 226

Qy      136 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 195
          |||
Db      227 GAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG 286

Qy      196 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG 255
          |||
Db      287 CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGACATGCCCAAGACTCAG 346

Qy      256 AAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---GAGAAGGAAAGGAAGT 312
          |||
Db      347 AAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGGAGAAGGAAAGGAAGT 406

```


tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 125 a 134 c 119 g 149 t
ORIGIN

Query Match 58.0%; Score 299.8; DB 9; Length 527;
Best Local Similarity 85.5%; Pred. No. 4.9e-69;
Matches 413; Conservative 0; Mismatches 17; Indels 53; Gaps 5;

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Qy      39 TCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTC 98
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Qy      99 CAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGA 158
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Db      467 CAGCAGTCGGAGGGCGCCTAAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGA 408

Qy     159 TCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGT 218
        |||
Db      407 TCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGT 348

Qy     219 CCGTGCCCGAGCGCCACACCGACATGCCAAGACCCAGAAGTATCAGCCCCCATCTACCAA 278
        |||
Db      347 CCGTGCCCGAGCGCCACACCGACATGCCAAGACCCAG----- 311

Qy     279 CAAGAACACGAAGTCTCAGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGA 338
        |||
Db      310 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGA 277

Qy     339 GTGCAGGAAACAAGAAGTACAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAG 397
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Db      276 GTGCAGGAAACAAGAAGTACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACAT 217

Qy     398 GCCACCGCAGGACCCTTTGCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAA 455
        |||
Db      216 GCCACCGCAGGATCCTTTGCTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAA 157

Qy     456 AAAATAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAA 514
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Db      156 AAAATAAGTTTGATAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAA 97

Qy     515 CAT 517
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Db      96 CAT 94

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RESULT 13
AI876493/c

LOCUS AI876493 642 bp mRNA linear EST 21-JUL-1999
DEFINITION uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1924219 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH
FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI876493
 VERSION AI876493.1 GI:5550542
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:980511
 Seq primer: custom primer used
 High quality sequence stop: 257.
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 /organism="Mus musculus"
 /mol_type="mRNA"
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 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
 primer CGACCTGCAGCTCGAGCACA."
 BASE COUNT 127 a 154 c 175 g 185 t 1 others
 ORIGIN
 Query Match 56.0%; Score 289.6; DB 9; Length 642;
 Best Local Similarity 78.9%; Pred. No. 2.7e-66;
 Matches 397; Conservative 0; Mismatches 95; Indels 11; Gaps 4;

Qy	2	GACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGCTGTGTGGAGACA	61
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Qy	62	GGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGA	121
Db	443	GGGGCTTTTCTTCAACAAGGCCACAGGCTATGGCTCCAGCATTTGGAGGGGCACCTCAGA	384
Qy	122	CAGGCATCGTGGATGAGTGCTGCTTCCGG-AGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	383	CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC	324
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	323	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC	264
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACCGAAGTCTCA---G	297
Db	263	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	204
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	203	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	144
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	143	CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG	84
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC	470
Db	83	CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA	24
Qy	471	ACATTTCAAAGATGGCATTTC	493
Db	23	ACATTACAAAGATGGGCATTTC	1

National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements

Seq primer: M13 Forward
 POLYA=Yes.

FEATURES	Location/Qualifiers
source	1. .499
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	/strain="C57BL/6J"
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	/clone="UI-M-BH3-auy-g-11-0-UI"
	/dev_stage="27-32 days"
	/lab_host="DH10B (Life Technologies)"
	/clone_lib="NIH_BMAP_M_S4"
	/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
	TAG_LIB=NIH_BMAP_M_S4
	TAG_TISSUE=pineal-glands

TAG_SEQ=CAGAC"
 BASE COUNT 86 a 112 c 124 g 177 t
 ORIGIN

Query Match 55.6%; Score 287.4; DB 9; Length 499;
 Best Local Similarity 80.8%; Pred. No. 9.7e-66;
 Matches 387; Conservative 0; Mismatches 81; Indels 11; Gaps 4;

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Db      499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGA 440

Qy     110 GGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGC 169
          |||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy     170 TGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGC 229
          |||||  ||  ||  ||  ||  |||||  ||  ||  |||  |||||  |||||  |||||
Db     379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy     230 GCCACACCGACATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGA 289
          |||||  |||||  |||||  |||||  |||||  ||  ||  |||  |||  |||||  |||||
Db     319 GCCCACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy     290 AGTCTCA---GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 346
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Db     259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy     347 AACAGAAGTACAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC 405
          |||||  |||||  |||||  ||  ||  |||  ||  |||  ||  ||  ||  |||||
Db     199 AACAGACCTACAGAATGTAGGAGGAGCCTCCACCGAGCAGAAAATGCCACATCACCGC 140

Qy     406 AGGACCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAA 459
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Db     139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy     460 TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          ||||  ||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      79 TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACAT 21
  
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RESULT 15
 AI169770/c

LOCUS AI169770 468 bp mRNA linear EST 20-JAN-1999
 DEFINITION EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
 RLIAT07 3' end, mRNA sequence.
 ACCESSION AI169770
 VERSION AI169770.1 GI:3709810
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 468)
 AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Kerlavage,A.R. and Adams,M.D.

```

TITLE      Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
           Gene Index
JOURNAL    Unpublished
COMMENT    Other_ESTs: TC50779
           Contact: Lee, NH
           The Institute for Genomic Research
           9712, Medical Center Drive, Rockville, MD 20850, USA
           Tel: (301)-838-3529
           Fax: (301)-838-0208
           Email: nhlee@tigr.org
           Seq primer: M13-21.

FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="ATCC (inhost):2027570"
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            /clone="RLIAT07"
            /clone_lib="Normalized rat liver, Bento Soares"
            /note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI;
            Site_2: NotI"

BASE COUNT      85 a      115 c      119 g      149 t
ORIGIN

Query Match          53.4%;  Score 276;  DB 9;  Length 468;
Best Local Similarity 80.5%;  Pred. No. 1e-62;
Matches 375;  Conservative 0;  Mismatches 80;  Indels 11;  Gaps 4;

Qy      63  GGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGAC 122
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Db      468 GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCACAGAC 409

Qy      123 AGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTG 182
         ||||| ||||||||||| ||||| ||||||||||||||| ||||| ||||||||||| ||
Db      408 GGGCATTGTGGATGAGTGTTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy      183 CGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACAT 242
         || || || ||||||| | ||||||||||| || ||||| ||||||||||||||| |||||
Db      348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGGCCAGCGCCACACTGACAT 289

Qy      243 GCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---GAG 299
         ||||||||| ||||||| ||||||| ||| || ||||||| | |||| || |||
Db      288 GCCCAAGACTCAGAAGTCCCAGCCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229

Qy      300 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 359
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Db      228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169

Qy      360 GGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 418
         | ||||| || || ||| ||||| | || | || | ||||||| || |||||||
Db      168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTGCT 109

Qy      419 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCAC 472
         | |||||| ||||| ||| ||| ||||| || ||| ||||| || |
Db      108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy      473 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517

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Db ||||| ||| ||||||||| |||||||||||||||||
48 ATTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 3

Search completed: December 13, 2003, 07:29:47
Job time : 1690.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2309.97 Seconds
(without alignments)
9156.102 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacagaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	517	100.0	517	6	AX147742	AX147742 Sequence
2	517	100.0	517	6	AX300779	AX300779 Sequence
3	467.4	90.4	523	6	AX147746	AX147746 Sequence
4	467.4	90.4	523	6	AX300783	AX300783 Sequence
5	377.2	73.0	471	6	AX147754	AX147754 Sequence
6	377.2	73.0	471	6	AX300791	AX300791 Sequence
7	355.4	68.7	444	9	HSU40870	U40870 Human alter
8	344.2	66.6	616	9	HSIGF1A	X56773 H.sapiens m
9	344.2	66.6	7260	6	AX375028	AX375028 Sequence
10	344.2	66.6	7260	6	AX411095	AX411095 Sequence
11	344.2	66.6	7260	9	HSIGFACI	X57025 Human IGF-I
12	342.6	66.3	666	6	A29119	A29119 H.sapiens I
13	342.6	66.3	725	9	HSIGFI	X00173 Homo sapien
14	342.6	66.3	728	9	HUMGFII	M29644 Human insul
15	342.6	66.3	1076	9	HUMIGFI	M27544 Human insul
16	341	66.0	620	6	I08370	I08370 Sequence 2
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18	330	63.8	798	10	RNIGFI2	X06108 Rat mRNA (c
19	330	63.8	958	10	RNIGFI1	X06107 Rat mRNA (c
20	326.8	63.2	710	10	RATIGFIA	M15480 Rat insulin
21	325.2	62.9	539	6	AX147744	AX147744 Sequence
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23	318.2	61.5	651	10	MMIGFIBR	X04482 Mouse mRNA
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29	286.4	55.4	3599	6	BD063790	BD063790 Insulin-1
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36	281.2	54.4	567	4	PIGGFIIA	M31175 Pig insulin
37	276	53.4	1284	4	BTILGF1A	X15726 Bovine mRNA
38	271.2	52.5	978	4	GOTIGFI	D11378 Goat mRNA f
39	271.2	52.5	978	6	E05279	E05279 DNA encodin
40	267.6	51.8	836	10	CPIGF1	X52951 Guinea pig
41	264.8	51.2	747	4	SHPIGFIA6	M31735 Sheep insul
42	264.8	51.2	790	4	SHPIGFIA21	M31734 Sheep insul
43	264.8	51.2	1015	4	SHPIGFIA46	M31736 Sheep insul
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45	258.4	50.0	317	6	AX147750	AX147750 Sequence

ALIGNMENTS

RESULT 1

AX147742

LOCUS AX147742 517 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 1 from Patent WO0136483.

ACCESSION AX147742

VERSION AX147742.1 GI:14346787

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 1 25-MAY-2001;
University College London (GB)

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"

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BASE COUNT 150 a 130 c 139 g 98 t

ORIGIN

Query Match 100.0%; Score 517; DB 6; Length 517;

Best Local Similarity 100.0%; Pred. No. 4.4e-155;

Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC  60
Qy      61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG  120
Qy     121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT  180
Qy     181  TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC  240
Qy     241  ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA  300
Qy     301  AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG  360
Qy     361  GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT  420
Qy     421  GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA  480
Qy     481  GATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT  517
        ||||||||||||||||||||||||||||||||||||
Db     481  GATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT  517

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RESULT 2

AX300779

LOCUS AX300779 517 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 1 from Patent WO0185781.

ACCESSION AX300779

VERSION AX300779.1 GI:17382060

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;
University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES Location/Qualifiers

source 1. .517
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

CDS <1. .333
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD13040.1"
 /db_xref="GI:17382061"
 /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNKTSQRRK
 GSTFEEHK"
 BASE COUNT 150 a 130 c 139 g 98 t
 ORIGIN

Query Match 100.0%; Score 517; DB 6; Length 517;
 Best Local Similarity 100.0%; Pred. No. 4.4e-155;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Qy	301	AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	301	AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Qy	361	GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT	420
Db	361	GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT	420
Qy	421	GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA	480
Db	421	GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA	480
Qy	481	GATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	517
Db	481	GATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	517

RESULT 3

AX147746

LOCUS AX147746 523 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 5 from Patent WO0136483.

ACCESSION AX147746


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Qy      358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
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Db      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy      417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
          |||
Db      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy      477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
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Db      481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521

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RESULT 4

AX300783

LOCUS AX300783 523 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 5 from Patent WO0185781.

ACCESSION AX300783

VERSION AX300783.1 GI:17382064

KEYWORDS .

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES Location/Qualifiers

source

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/organism="Oryctolagus cuniculus"

/mol_type="genomic DNA"

/db_xref="taxon:9986"

CDS

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/note="unnamed protein product"

/codon_start=1

/protein_id="CAD13042.1"

/db_xref="GI:17382065"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV
DECCFRSCDLRRLEMYCAPLKPAAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR
KGSTFEEHK"

BASE COUNT 154 a 129 c 142 g 98 t

ORIGIN

Query Match 90.4%; Score 467.4; DB 6; Length 523;

Best Local Similarity 96.2%; Pred. No. 4.4e-139;

Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

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Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

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Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
 || |||
 Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
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 Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Qy 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 357
 |||
 Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360
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 Qy 358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
 |||
 Db 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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 Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
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 Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
 |||
 Qy 477 CAAAGATGGCATTTCCTCCAATGAAATACACAAGTAAACAT 517
 |||
 Db 481 CAAAGATGGCATTTCCTCCAATGAAATACACAAGTAAACAT 521
 |||

RESULT 5

AX147754

LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001

DEFINITION Sequence 13 from Patent WO0136483.

ACCESSION AX147754

VERSION AX147754.1 GI:14348552

KEYWORDS .

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001; University College London (GB)

FEATURES Location/Qualifiers

source 1..471
 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9986"
 CDS <1..318
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41264.1"
 /db_xref="GI:14348553"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV
DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
YRM"

BASE COUNT 132 a 118 c 131 g 90 t
ORIGIN

Query Match 73.0%; Score 377.2; DB 6; Length 471;
Best Local Similarity 87.8%; Pred. No. 5.4e-110;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
          ||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          |||
Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||
Db    256 ----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy    361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          |||
Db    312 GATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 371

Qy    420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 479
          |||
Db    372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 431

Qy    480 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
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Db    432 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 469
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RESULT 6

AX300791

LOCUS AX300791 471 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 13 from Patent W00185781.

ACCESSION AX300791

VERSION AX300791.1 GI:17382072

KEYWORDS .

SOURCE *Oryctolagus cuniculus* (rabbit)

ORGANISM *Oryctolagus cuniculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 431

Qy 480 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
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Db 432 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 469

RESULT 7

HSU40870

LOCUS HSU40870 444 bp mRNA linear PRI 05-APR-1996

DEFINITION Human alternatively spliced human insulin-like growth factor-I
 (IGF-I) mRNA, partial cds.

ACCESSION U40870

VERSION U40870.1 GI:1100902

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 444)

AUTHORS Chew,S.L., Lavender,P., Clark,A.J. and Ross,R.J.

TITLE An alternatively spliced human insulin-like growth factor-I
 transcript with hepatic tissue expression that diverts away from
 the mitogenic IBEL peptide

JOURNAL Endocrinology 136 (5), 1939-1944 (1995)

MEDLINE 95237119

PUBMED 7720641

REFERENCE 2 (bases 1 to 444)

AUTHORS Chew,S.L.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-1995) Shern L. Chew, Endocrinology, St
 Bartholomew's Hospital Medical College, West Smithfield, London,
 Ec1A 7Be, UK

FEATURES Location/Qualifiers

source 1..444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="pC4"
 /tissue_type="liver"

gene 1..444
 /gene="IGF-I"

CDS <1..420
 /gene="IGF-I"
 /note="alternatively spliced; previously, exon 5 and 6
 were thought to be mutually exclusive; this transcript
 splices from exon 5 into exon 6; the alternatively spliced
 transcript would continue with exon 5 to the polyA signal"
 /codon_start=1
 /product="insulin-like growth factor-I"
 /protein_id="AAA96152.1"
 /db_xref="GI:1100903"
 /translation="LKVKMHTMSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQ
 FVCGDRGFYFNKPTGYGSSRRAPQTGIVDECCFRSCDLRRLRLEMYCAPLKPASARSV
 RAQRHTDMPKTQKYQPPSTNKNKTSQRRKGSTFEERK"

exon 1..6
 /gene="IGF-I"

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                /number=4
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                /gene="IGF-I"
                /number=5
    exon          395. .420
                /gene="IGF-I"
                /number=6
BASE COUNT      107 a    125 c    125 g    87 t
ORIGIN

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Query Match          68.7%;  Score 355.4;  DB 9;  Length 444;
Best Local Similarity 99.7%;  Pred. No. 5.7e-103;
Matches 356;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      88 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 147

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db    148 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 207

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db    208 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 267

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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Db    268 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 327

Qy    241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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Db    328 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 387

Qy    301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
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Db    388 AGGAAAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 444

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RESULT 8
HSIGF1A
LOCUS      HSIGF1A                      616 bp    mRNA    linear    PRI_29-NOV-1993
DEFINITION H.sapiens mRNA for IGF-1a.
ACCESSION  X56773 S61841
VERSION    X56773.1 GI:32989
KEYWORDS   IGF-1 gene.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 616)

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AUTHORS Sandberg-Nordqvist,A.C., Stahlbom,P.A., Lake,M. and Sara,V.R.
 TITLE Characterization of two cDNAs encoding insulin-like growth factor 1 (IGF-1) in the human fetal brain
 JOURNAL Brain Res. Mol. Brain Res. 12 (1-3), 275-277 (1992)
 MEDLINE 92186627
 PUBMED 1372070
 REFERENCE 2 (bases 1 to 616)
 AUTHORS Sandberg Nordqvist,A.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1990) A.C.Sandberg Nordqvist, KAROLINSKA INST'S DEPT OF PATHOLOGY, KAROLINSKA HOSPITAL, BOX 605 00, S-104 01 STOCKHOLM, SWEDEN
 REFERENCE 3 (bases 1 to 616)
 AUTHORS Sandberg-Nordqvist,A.C., Stahlbom,P.A., Reinecke,M., Collins,V.P., von Holst,H. and Sara,V.
 TITLE Characterization of insulin-like growth factor 1 in human primary brain tumors
 JOURNAL Cancer Res. 53 (11), 2475-2478 (1993)
 MEDLINE 93265440
 PUBMED 8495408
 FEATURES Location/Qualifiers
 source 1. .616
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="12"
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 /tissue_type="brain"
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 /db_xref="SWISS-PROT:P01343"
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 exon 403. .616
 /note="exon 5"
 BASE COUNT 159 a 158 c 160 g 139 t
 ORIGIN

Query Match 66.6%; Score 344.2; DB 9; Length 616;
 Best Local Similarity 87.3%; Pred. No. 2.5e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 145 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 204

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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 Db 205 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 264
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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 Db 265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 324
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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 Db 325 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 384
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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 Db 385 ATGCCCAAGACCCAG----- 399
 Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
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 Db 400 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 455
 Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
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 Db 456 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 515
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTT 477
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 Db 516 TGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 575
 Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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 Db 576 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 616

RESULT 9

AX375028

LOCUS AX375028 7260 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 31 from Patent WO0210436.

ACCESSION AX375028

VERSION AX375028.1 GI:19169860

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baak, J. and Mutter, G.L.

TITLE Prognostic classification of breast cancer

JOURNAL Patent: WO 0210436-A 31 07-FEB-2002;

THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)

FEATURES

Location/Qualifiers

source

1. .7260

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 2330 a 1415 c 1240 g 2275 t

ORIGIN

Query Match 66.6%; Score 344.2; DB 6; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 3.6e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
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Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
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Db     566 ----AAGGAAGTACATTTGAAGAACCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        ||||| ||||||||| ||||||||||||| |||| ||||||||||| |||||||||
Db     622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
        ||||| ||||||||| ||||| ||||| ||| ||||||||||||| |||||||
Db     682 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 741

Qy     478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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Db     742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782
  
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RESULT 10

AX411095

LOCUS AX411095 7260 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 3742 from Patent WO0229103.

ACCESSION AX411095

VERSION AX411095.1 GI:21443800

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.

TITLE Gene expression profiles in liver cancer

JOURNAL Patent: WO 0229103-A 3742 11-APR-2002;

GENE LOGIC INC (US)

FEATURES Location/Qualifiers
 source 1. .7260
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="EMBL/GenBank Accession No. X57025"

BASE COUNT 2330 a 1415 c 1240 g 2275 t
 ORIGIN

Query Match 66.6%; Score 344.2; DB 6; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 3.6e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db      371  AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121  ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db     431  ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181  TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          |||
Db     491  TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241  ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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Db     551  ATGCCCAAGACCCAG----- 565

Qy     301  AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||
Db     566  ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361  GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          |||
Db     622  GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420  TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
          |||
Db     682  TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 741

Qy     478  AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          |||
Db     742  AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782
  
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RESULT 11

HSIGFACI

LOCUS HSIGFACI 7260 bp mRNA linear PRI 17-FEB-1992
 DEFINITION Human IGF-I mRNA for insulin-like growth factor I.
 ACCESSION X57025
 VERSION X57025.1 GI:33007
 KEYWORDS insulin-like growth factor I.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 7260)

AUTHORS Steenbergh, P.H., Koonen-Reemst, A.M., Cleutjens, C.B. and
Sussenbach, J.S.

TITLE Complete nucleotide sequence of the high molecular weight human
IGF-I mRNA

JOURNAL Biochem. Biophys. Res. Commun. 175 (2), 507-514 (1991)

MEDLINE 91207342

PUBMED 2018498

REFERENCE 2 (bases 1 to 7260)

AUTHORS Steenbergh, P.H.

TITLE Direct Submission

JOURNAL Submitted (18-DEC-1990) P.H. Steenbergh, LAB FOR PHYSIOLOGICAL
CHEMISTRY, UNIVERSITY OF UTRECHT, VONDELLAAN 24 A, 3521 GG UTRECHT,
THE NETHERLANDS

FEATURES Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12 q22-24.1"
/tissue_type="liver"
/dev_stage="adult"

gene 1. .7260
/gene="IGF-I"

mRNA 1. .7260
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exon 1. .229
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CDS 167. .628
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/evidence=experimental

mat_peptide 311. .520
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/evidence=experimental

exon 230. .386
/gene="IGF-I"
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/evidence=experimental

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exon          387. .568
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               /number=3
               /evidence=experimental
exon          569. .7236
               /gene="IGF-I"
               /number=5
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polyA_signal  861. .865
               /gene="IGF-I"
               /note="1.1 kb mRNA"
               /evidence=experimental
repeat_unit   3986. .4026
               /gene="IGF-I"
               /note="CA-repeat"
               /evidence=experimental
repeat_unit   5926. .6215
               /gene="IGF-I"
               /evidence=experimental
               /rpt_family="AluI"
polyA_signal  7205. .7210
               /gene="IGF-I"
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               /evidence=experimental
BASE COUNT    2330 a    1415 c    1240 g    2275 t
ORIGIN

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Query Match          66.6%; Score 344.2; DB 9; Length 7260;
Best Local Similarity 87.3%; Pred. No. 3.6e-99;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
          |||
Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
          |||
Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550
          |||
Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          |||
Db      551 ATGCCCAAGACCCAG----- 565
          |||
Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||
Db      566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621
          |||
Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
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Db          622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681
Qy          420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
              ||||| ||||| ||||| ||||| |||  ||||| ||||| ||||| |||||
Db          682 TGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 741
Qy          478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
              ||||| |||  ||||| ||||| ||||| ||||| ||||| |||||
Db          742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782

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RESULT 12

A29119

LOCUS A29119 666 bp DNA linear PAT 15-JUN-1995

DEFINITION H.sapiens IGF1 gene fragment from patent GB2241703.

ACCESSION A29119

VERSION A29119.1 GI:1247520

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 666)

AUTHORS .

JOURNAL Patent: GB 2241703-A 3 11-SEP-1991;

FEATURES Location/Qualifiers

source 1. .666

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

CDS 25. .384

/partial

/codon_start=1

/product="IGF-1 precursor"

/protein_id="CAA01955.1"

/db_xref="GI:4529932"

/translation="MALCLLTFTSSATAGPETLCGAELVDALQFVCGDRGFYFNKPTG
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HLKNASRGSAGNKNYRM"

mat_peptide 67. .276

/product="IGF-1"

BASE COUNT 173 a 167 c 181 g 145 t

ORIGIN

Query Match 66.3%; Score 342.6; DB 6; Length 666;

Best Local Similarity 87.1%; Pred. No. 8.2e-99;

Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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Qy          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db          67 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 126
Qy          61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          127 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 186
Qy          121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

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Db      187 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 246
Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
      ||||||||||||||||||||||||||||||||||||||||||||
Db      247 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 306
Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
      |||||||||||||||
Db      307 ATGCCCAAGACCCAG----- 321
Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
      ||||||||||||||||||||||||||||||||||||||||||||
Db      322 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 377
Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
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Db      378 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 437
Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGCCAAAAAATAAGTTTGATCACATTTTC 477
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Db      438 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 497
Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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Db      498 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 538

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RESULT 13

HSIGFI

LOCUS HSIGFI 725 bp mRNA linear PRI 11-DEC-1998

DEFINITION Homo sapiens mRNA for insulin-like growth factor 1A precursor, complete CDS.

ACCESSION X00173

VERSION X00173.1 GI:33015

KEYWORDS growth factor; insulin super family; insulin-like growth factor I; signal peptide; somatomedin.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Jansen,M., van Schaik,F.M., Ricker,A.T., Bullock,B., Woods,D.E., Gabbay,K.H., Nussbaum,A.L., Sussenbach,J.S. and Van den Brande,J.L.

TITLE Sequence of cDNA encoding human insulin-like growth factor I precursor

JOURNAL Nature 306 (5943), 609-611 (1983)

MEDLINE 84068210

PUBMED 6358902

COMMENT Data kindly reviewed (28-MAY-1984) by M. Jansen.

FEATURES Location/Qualifiers

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    gene        1. .725
                  /gene="IGF-1"

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CDS                12. .473
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                   /db_xref="SWISS-PROT:P01343"
                   /translation="MGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYLALCLLTFTS
polyA_site         725
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BASE COUNT        190 a    174 c    183 g    178 t
ORIGIN

Query Match          66.3%; Score 342.6; DB 9; Length 725;
Best Local Similarity 87.1%; Pred. No. 8.3e-99;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      216 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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Db      276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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Db      336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 395

Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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Db      396 ATGCCCAAGACCCAG----- 410

Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
        ||||||||||||||| ||||||||||||||| |||||||||||||||
Db      411 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 466

Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        ||||| ||||||||| ||||||||||||| |||| ||||||||||| ||||||||
Db      467 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 526

Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
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Db      527 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 586

Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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Db      587 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 627

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HUMGFII
 LOCUS HUMGFII 728 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human insulin-like growth factor I mRNA, complete cds.
 ACCESSION M29644
 VERSION M29644.1 GI:183119
 KEYWORDS insulin-like growth factor.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 728)
 AUTHORS Rall,L.B., Scott,J. and Bell,G.I.
 TITLE Human insulin-like growth factor I and II messenger RNA: isolation
 of complementary DNA and analysis of expression
 JOURNAL Meth. Enzymol. 146, 239-248 (1987)
 MEDLINE 88065102
 PUBMED 3683205
 COMMENT Original source text: Human (adult) liver, cDNA to mRNA.
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 /db_xref="taxon:9606"
 /map="12q23"
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 CDS 81..473
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 /product="insulin-like growth factor I"
 BASE COUNT 193 a 174 c 183 g 178 t
 ORIGIN Chromosome 12q23.

Query Match 66.3%; Score 342.6; DB 9; Length 728;
 Best Local Similarity 87.1%; Pred. No. 8.3e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215
 Qy 61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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 Db 216 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy 121 ACAGGCATCGTGGATGAGTGCCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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 Db 276 ACAGGTATCGTGGATGAGTGCCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy 181 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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 Db 336 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 395

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
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 Db 396 ATGCCCAAGACCCAG----- 410

Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
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 Db 411 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 466

Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
 ||||| ||||||||| ||||||||| ||| ||||||||| |||||||||
 Db 467 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 526

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGCCAAAAAATAAGTTTGATCACATTTTC 477
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 Db 527 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 586

Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 ||||| ||| |||||||||||||||||||||||||
 Db 587 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 627

RESULT 15

HUMIGFI

LOCUS HUMIGFI 1076 bp mRNA linear PRI 08-NOV-1994

DEFINITION Human insulin-like growth factor mRNA, complete cds.

ACCESSION M27544

VERSION M27544.1 GI:184829

KEYWORDS insulin-like growth factor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1076)

AUTHORS Le Bouc,Y., Dreyer,D., Jaeger,F., Binoux,M. and Sondermeyer,P.

TITLE Complete characterization of the human IGF-I nucleotide sequence isolated from a newly constructed adult liver cDNA library

JOURNAL FEBS Lett. 196 (1), 108-112 (1986)

MEDLINE 86108910

PUBMED 2935423

COMMENT Original source text: Human liver, cDNA to mRNA, clones lanbda-TG[03,04,05].

FEATURES Location/Qualifiers

source 1. .1076
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 /db_xref="taxon:9606"
 /map="7p13-p12"
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 /gene="IGFBP1"

mRNA <1. .>1076
 /gene="IGFBP1"
 /note="IGF mRNA (alt.)"
 mRNA <1. .989
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Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	517	100.0	517	22	AAD06398	Human IGF-I isoform
2	517	100.0	517	24	AAS16877	Human mechano-grow
3	467.4	90.4	523	22	AAD06400	Rabbit IGF-I isoform
4	467.4	90.4	523	24	AAS16879	Rabbit mechano-grow
5	467.4	90.4	553	18	AAT84893	Rabbit insulin-like
6	377.2	73.0	471	22	AAD06405	Rabbit liver-type
7	377.2	73.0	471	24	AAS16884	Rabbit insulin-like
8	344.2	66.6	818	8	AAN70436	Sequence encoding
9	344.2	66.6	7260	24	ABT11091	Human breast cancer
10	344.2	66.6	7260	24	ABK84583	Human cDNA difference
11	344.2	66.6	7260	24	ABN97244	Gene #3742 used to
12	344.2	66.6	7260	24	ABK64812	Human benign prostate
13	344.2	66.6	7260	24	ABK35504	Human endometrial
14	344.2	66.6	7260	24	ABK35561	Gene IGF1 difference
15	342.6	66.3	777	18	AAT84894	Human insulin-like
16	339.4	65.6	622	7	AAN60490	Human prepro-somat
17	325.2	62.9	539	22	AAD06399	Rat IGF-I isoform
18	325.2	62.9	539	24	AAS16878	Rat mechano-growth
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20	308.6	59.7	1136	8	AAN70435	Sequence encoding
21	286.4	55.4	3599	19	AAV50428	Plasmid pIG0552 loop
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27	285.4	55.2	612	22	AAS14695	Human cDNA encoding
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39	247.8	47.9	487	22	AAD06404	Rat liver-type IGF
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41	234.2	45.3	671	24	ABT09479	Phase-1 Rat CT gen
42	210	40.6	210	24	AAD45568	Human insulin-like
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ALIGNMENTS

RESULT 1

AAD06398

ID AAD06398 standard; cDNA; 517 BP.

XX

AC AAD06398;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..333

FT /*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02447.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth

PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a

PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 49-50; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),

CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a

CC medicament for the treatment of neurological disorder. The MGF is capable

CC of reducing motoneurone loss by 20% or greater in response to nerve

CC avulsion, and effects motoneurone rescue, preferably adult motoneurone

CC rescue. The MGF polynucleotide and polypeptide are useful in the

CC manufacture of a medicament for the treatment of a neurological disorder,

CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 22; Length 517;
 Best Local Similarity 100.0%; Pred. No. 1.6e-146;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	421	GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA	480
Db	421	GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA	480
Qy	481	GATGGCATTTCCCCCAATGAAATACACAAGTAAACAT	517
Db	481	GATGGCATTTCCCCCAATGAAATACACAAGTAAACAT	517

RESULT 2
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 ID AAS16877 standard; cDNA; 517 BP.
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 AC AAS16877;
 XX
 DT 25-FEB-2002 (first entry)
 XX
 DE Human mechano-growth factor (MGF) cDNA.
 XX
 KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /*tag= a
 FT /product= "Human MGF"
 FT /partial
 FT /note= "No start codon"
 FT exon 1..76
 FT /*tag= b
 FT /number= 3
 FT exon 77..259
 FT /*tag= c
 FT /number= 4
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 FT /*tag= d
 FT /number= 5
 FT exon 308..330
 FT /*tag= e
 FT /number= 6
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 PN WO200185781-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-GB02054.
 XX
 PR 10-MAY-2000; 2000GB-0011278.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX
 PI Goldspink G, Terenghi G;
 XX
 DR WPI; 2002-055585/07.
 DR P-PSDB; AAU10559.
 XX
 PT Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to
 PT treat nerve damage -
 XX

PS Claim 11; Fig 5; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the human MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 24; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.6e-146;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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Qy    361 GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT 420
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Qy    421 GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 480
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RESULT 3

AAD06400

ID AAD06400 standard; cDNA; 523 BP.

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AC AAD06400;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02449.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth

PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a

PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 53-54; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),

CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a

CC medicament for the treatment of neurological disorder. The MGF is capable

CC of reducing motoneurone loss by 20% or greater in response to nerve

CC avulsion, and effects motoneurone rescue, preferably adult motoneurone

CC rescue. The MGF polynucleotide and polypeptide are useful in the

CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
 CC injury that affects motoneurons, motoneuron loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 22; Length 523;
 Best Local Similarity 96.2%; Pred. No. 1.8e-131;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Db	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Qy	358	CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
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Qy	477	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	517
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RESULT 4

AAS16879

ID AAS16879 standard; cDNA; 523 BP.

XX

AC AAS16879;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KW nerve avulsion.

XX

OS Oryctolagus cuniculus.

XX

Key	Location/Qualifiers
FT CDS	1..336
FT	/*tag= a
FT	/product= "Rabbit MGF"
FT	/partial
FT	/note= "No start codon"
FT exon	1..76
FT	/*tag= b
FT	/number= 3
FT exon	77..259
FT	/*tag= c
FT	/number= 4
FT exon	260..309
FT	/*tag= d
FT	/number= 5
FT exon	311..333
FT	/*tag= e
FT	/number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10561.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -

PS Disclosure; Fig 7; 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACCGAAGTCTCA---G	297
Db	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	476
Db	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Qy	477	CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT	517

Db 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521

RESULT 5

AAT84893

ID AAT84893 standard; cDNA; 553 BP.

XX

AC AAT84893;

XX

DT 14-APR-1998 (first entry)

XX

DE Rabbit insulin like growth factor 1 encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;

KW heart; neuromuscular disease; primer; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..366

FT /*tag= a

FT /product= "IGF-1"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23301.

XX

PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 3; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.

SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC	60
Db	31	GGACCGGAGACGCTCTGCGGGTGTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC	90
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	91	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	150
Qy	121	ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	151	ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	210
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	211	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	270
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	271	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	330
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	331	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	390
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	391	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	450
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	476
Db	451	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	510
Qy	477	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	517
Db	511	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	551

AAD06405

XX

XX

XX

XX

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..318
 FT /*tag= a
 FT /product= "Liver-type IGF-I isoform (L.IGF-I)"
 FT /transl_except= (pos:7..9, aa:Gln)
 FT /transl_except= (pos:25..27, aa:Gln)
 FT /note= "These translation exceptions occur while decoding
 FT the alternative version of the protein (AAE02456).
 FT The CDS comprises exons 3, 4 and 6 and
 FT does not include start codon"
 FT /partial
 XX
 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02452, AAE02456.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Disclosure; Page 59-60; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
 CC The L.IGF-I protein comprises amino acid sequences encoded by

CC nucleic acid sequence of IGF-I exons 4 and 6.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 73.0%; Score 377.2; DB 22; Length 471;

Best Local Similarity 87.8%; Pred. No. 3.8e-104;

Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db    121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        ||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
        |||
Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
        |||
Db    256 ----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy    361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        |||
Db    312 GATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 371

Qy    420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 479
        |||
Db    372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 431

Qy    480 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
        |||
Db    432 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 469
```

RESULT 7

AAS16884

ID AAS16884 standard; cDNA; 471 BP.

XX

AC AAS16884;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
neuroprotective; nerve damage; peripheral nervous system; nerve severing;

KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Rabbit L.IGF-I"
FT /partial
FT /note= "No start codon"
FT exon 1..75
FT /*tag= b
FT /number= exon 3
FT exon 76..258
FT /*tag= c
FT /number= exon 4
FT exon 259..315
FT /*tag= d
FT /number= exon 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10564.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
PS Disclosure; Fig 10; 65pp; English.
XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like

CC growth factor I liver-type isoform (L.IGF-I) used in experiments on
CC motoneuron loss.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 73.0%; Score 377.2; DB 24; Length 471;
Best Local Similarity 87.8%; Pred. No. 3.8e-104;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        ||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
        |||
Db    241 ATGCCCCAAGACTCAG----- 255

Qy    301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
        |||
Db    256 ----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy    361 GATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        |||
Db    312 GATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 371

Qy    420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 479
        |||
Db    372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 431

Qy    480 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
        |||
Db    432 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 469
```

RESULT 8

AAN70436

ID AAN70436 standard; cDNA; 818 BP.

XX

AC AAN70436;

XX

DT 25-MAR-2003 (updated)

DT 05-APR-1991 (first entry)

XX

DE Sequence encoding insulin-like growth factor 1A (IGF-1A).

XX

KW Growth promoter; lactation enhancer; cell proliferation; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP229750-A.
 XX
 PD 22-JUL-1987.
 XX
 PF 06-JAN-1987; 87EP-0870001.
 XX
 PR 20-NOV-1986; 86US-0929671.
 PR 07-JAN-1986; 86US-0816662.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Krivi GG, Rotwein PS;
 XX
 DR WPI; 1987-200203/29.
 XX
 PT New pre-pro-insulin-like growth factor-1 protein - obtd. by
 PT recombinant DNA procedures for use as growth promoters for
 PT enhancing lactation, for stimulating cell proliferation etc.
 XX
 PS Example; Fig 5; 59pp; English.
 XX
 CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
 CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
 CC The radiolabeled 42 mer was then employed to screen for IGF-I
 CC containing DNA sequences in a human liver cDNA library. Insulin-
 CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
 CC library by using lambda gt 11 (AAN70435, AAN70436). The human IGF-1
 CC genomic gene was isolated and mapped. It encodes at least two
 CC preproinsulin-like growth factor-1 proteins. An essentially pure
 CC preproinsulin-like growth factor-1 protein comprising the sequence
 CC of amino acids shown in Figure six is claimed (AAP70277).
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 66.6%; Score 344.2; DB 8; Length 818;
 Best Local Similarity 87.3%; Pred. No. 4.8e-94;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

```

Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
      |||
Db      203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 262

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
      |||
Db      263 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
      |||
Db      323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy      181 TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
      |||

```

Db 383 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442
 Qy 241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 443 ATGCCCCAAGACCCAG----- 457
 Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||
 Db 458 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 513
 Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
 |||||
 Db 514 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 573
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTTGATCACATTTC 477
 |||||
 Db 574 TGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 633
 Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 634 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 674

RESULT 9

ABT11091

ID ABT11091 standard; cDNA; 7260 BP.

XX

AC ABT11091;

XX

DT 04-DEC-2002 (first entry)

XX

DE Human breast cancer associated coding sequence SEQ ID NO: 1225.

XX

KW Human; breast specific gene; breast cancer; differential expression;
 KW cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200259271-A2.

XX

PD 01-AUG-2002.

XX

PF 25-JAN-2002; 2002WO-US02176.

XX

PR 25-JAN-2001; 2001US-263757P.

PR 25-APR-2001; 2001US-286090P.

PR 23-MAY-2001; 2001US-292517P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Orr MS, Nation M, Diggans JC, Zeng W;

XX

DR WPI; 2002-674803/72.

XX

PT Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer -

PS Claim 1; SEQ ID NO 1225; 260pp + Sequence Listing; English.

CC The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT11112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.
CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention.

XX

Db

Ov

DD

Db

Ov

Db

Ov

Db

Ov

Db

Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 ||||| ||| |||||||||||||||||||||||||
 Db 742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782

RESULT 10

ABK84583

ID ABK84583 standard; cDNA; 7260 BP.

XX

AC ABK84583;

XX

DT 14-AUG-2002 (first entry)

XX

DE Human cDNA differentially expressed in granulocytic cells #1154.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.

XX

OS Homo sapiens.

XX

PN WO200228999-A2.

XX

PD 11-APR-2002.

XX

PF 03-OCT-2001; 2001WO-US30821.

XX

PR 03-OCT-2000; 2000US-237189P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

DR WPI; 2002-435328/46.

XX

PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -

XX

PS Claim 1; SEQ ID No 1154; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the

CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          |||||||||||||||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          ||||| ||||||| ||||||| |||| ||||| ||||| ||||| |||||
Db     622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTT 477
          ||||| ||||||| ||||| ||||| ||| ||||||||||||||| |||||
Db     682 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 741

Qy     478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          ||||| ||| |||||||||||||||||||||||||||||||
Db     742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782
```

RESULT 12

ABK64812

ID ABK64812 standard; DNA; 7260 BP.

XX

AC ABK64812;

XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #707.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 391-393; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.1e-93;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db     311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db     371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        |||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
        |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
        |||
Db     566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        |||
Db     622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTT 477
        |||
Db     682 TGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 741

Qy     478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
        |||
Db     742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782

```

RESULT 13

ABK35504

ID ABK35504 standard; DNA; 7260 BP.

XX

AC ABK35504;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human endometrial cancer related gene, IGF1.

XX

KW Human; ds; gene; endometrial cancer; differential expression;

KW DNA microarray; protein microarray.

XX

OS Homo sapiens.

XX

PN WO200209573-A2.

XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-US24104.
 XX
 PR 31-JUL-2000; 2000US-221735P.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Mutter GL;
 XX
 DR WPI; 2002-179967/23.
 DR P-PSDB; AAU84284.
 XX
 PT Diagnosing endometrial cancer comprises determining expression of
 PT nucleic acid molecules or expression products that are differentially
 PT expressed in normal and malignant endometrium -
 XX
 PS Claim 1; Page 85-89; 233pp; English.
 XX
 CC The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50
 CC nucleic acids bound to a solid substrate. Also included is a solid-phase
 CC protein microarray comprising at least 2 antibodies or its antigen
 CC binding fragments, that specifically bind at least 2 different
 CC polypeptides from the 50 fully defined sequences as given in the
 CC specification, fixed to a solid substrate. The methods and arrays are
 CC useful for the diagnosis of endometrial cancer, selecting and monitoring
 CC treatment regimes and identification of lead compounds useful for the
 CC treatment of endometrial cancer. The present sequence is one of 50
 CC genes differentially expressed between cancerous and non-cancerous
 CC samples.
 XX
 SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.1e-93;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

QY 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

QY 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

QY 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

```

          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCGCCACACCGAC 550
Qy      241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          ||||||||||||||||
Db      551 ATGCCCCAAGACCCAG----- 565
Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621
Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          |||||| |||||||| |||||||||||| ||| |||||||||||| ||||||||
Db      622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681
Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTC 477
          ||||| |||||||| |||| ||||| ||| |||||||||||| |||||
Db      682 TGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 741
Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          ||||| ||| ||||||||||||||||||||||||||||
Db      742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782

```

RESULT 14

ABK35561

ID ABK35561 standard; DNA; 7260 BP.

XX

AC ABK35561;

XX

DT 08-MAY-2002 (first entry)

XX

DE Gene IGF1 differentially expressed in breast cancer tissue.

XX

KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;

KW MAI; mitotic activity index; cytostatic; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200210436-A2.

XX

PD 07-FEB-2002.

XX

PF 27-JUL-2001; 2001WO-US23642.

XX

PR 28-JUL-2000; 2000US-222093P.

XX

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

PA (BAK/) BAK J.

XX

PI Baak J, Mutter GL;

XX

DR WPI; 2002-180084/23.

DR P-PSDB; AAU84341.

XX

PT Diagnosing breast cancer comprises determining expression of nucleic
PT acid molecules or expression products that are differentially expressed

QY 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 ||||| ||| ||||||||||||||||||||||||||||
 Db 742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782

RESULT 15

AAT84894

ID AAT84894 standard; cDNA; 777 BP.

XX

AC AAT84894;

XX

DT 14-APR-1998 (first entry)

XX

DE Human insulin like growth factor 1 Ea isoform encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
 KW heart; neuromuscular disease; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 26..496

FT /*tag= a

FT /product= "IGF-1 Ea isoform"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23302.

XX

PT Use of insulin like growth factor I characterised by presence of Ec
 PT peptide - to treat humans or animals, particularly muscle disorders,
 PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 4; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
 CC is characterised by the presence of the Ec peptide, or a functional
 CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
 CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
 CC Becker muscular dystrophy, autosomal dystrophies and related progressive
 CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
 CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
 CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
 CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
 CC heart failure or insult, specifically myocarditis or myocardial

CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes human
CC IGF-1 Ea isoform used in the present specification.

XX

SQ Sequence 777 BP; 201 A; 193 C; 204 G; 179 T; 0 other;

Query Match 66.3%; Score 342.6; DB 18; Length 777;
Best Local Similarity 87.1%; Pred. No. 1.4e-93;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db     179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
      |||
Db    239 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
      |||
Db    299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db    359 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 418

Qy    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
      |||
Db    419 ATGCCCAAGACCCAG----- 433

Qy    301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
      |||
Db    434 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 489

Qy    361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
      |||
Db    490 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 549

Qy    420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTT 477
      |||
Db    550 TGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 609

Qy    478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
      |||
Db    610 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 650
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Job time : 209.586 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55 ; Search time 47.8037 Seconds
(without alignments)
4773.589 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacaat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	467.4	90.4	553	3	US-09-142-583A-3	Sequence 3, Appli
2	467.4	90.4	553	3	US-09-142-583A-5	Sequence 5, Appli
3	342.6	66.3	777	3	US-09-142-583A-10	Sequence 10, Appl
4	339.4	65.6	622	6	5405942-2	Patent No. 5405942
5	286.4	55.4	5707	2	US-08-472-809B-8	Sequence 8, Appli
6	286.4	55.4	6345	2	US-08-472-809B-7	Sequence 7, Appli
7	255.2	49.4	357	6	5405942-13	Patent No. 5405942
8	253.6	49.1	357	6	5405942-9	Patent No. 5405942
9	208.4	40.3	210	6	5405942-7	Patent No. 5405942
10	208.4	40.3	210	6	5405942-11	Patent No. 5405942
11	208.4	40.3	2862	4	US-09-255-829-13	Sequence 13, Appl

12	206.8	40.0	210	6	5405942-15	Patent No. 5405942
13	202.8	39.2	240	1	US-08-308-196A-1	Sequence 1, Appli
14	202.8	39.2	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	202.8	39.2	390	3	US-09-029-267-13	Sequence 13, Appl
16	174.4	33.7	798	1	US-07-953-230A-6	Sequence 6, Appli
17	163.4	31.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	163.4	31.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	125.8	24.3	485	1	US-07-989-845-29	Sequence 29, Appl
20	125.8	24.3	485	1	US-07-989-844-13	Sequence 13, Appl
21	125.8	24.3	485	1	US-08-110-663-1	Sequence 1, Appli
22	125.8	24.3	485	1	US-08-169-688-1	Sequence 1, Appli
23	125.8	24.3	485	1	US-08-240-121-13	Sequence 13, Appl
24	125.8	24.3	485	1	US-08-451-241-13	Sequence 13, Appl
25	125.8	24.3	485	1	US-08-110-664-1	Sequence 1, Appli
26	125.8	24.3	485	1	US-08-446-882-1	Sequence 1, Appli
27	125.8	24.3	485	1	US-08-385-187A-1	Sequence 1, Appli
28	125.8	24.3	485	1	US-08-470-108-1	Sequence 1, Appli
29	125.8	24.3	485	5	PCT-US93-11297-13	Sequence 13, Appl
30	125.8	24.3	485	5	PCT-US93-11298-29	Sequence 29, Appl
31	123.8	23.9	621	3	US-08-989-251-40	Sequence 40, Appl
32	123.8	23.9	621	3	US-09-340-250-40	Sequence 40, Appl
33	123.8	23.9	621	4	US-09-528-108-40	Sequence 40, Appl
34	122	23.6	237	1	US-07-764-655D-8	Sequence 8, Appli
35	120.8	23.4	243	2	US-08-482-182-75	Sequence 75, Appl
36	120.4	23.3	233	1	US-08-444-142-3	Sequence 3, Appli
37	120.4	23.3	233	1	US-08-444-131-3	Sequence 3, Appli
c 38	120.4	23.3	237	1	US-07-764-655D-9	Sequence 9, Appli
39	120.4	23.3	717	1	US-08-284-784-40	Sequence 40, Appl
40	120.4	23.3	717	2	US-08-854-811-40	Sequence 40, Appl
41	120.4	23.3	783	1	US-08-284-784-43	Sequence 43, Appl
42	120.4	23.3	783	2	US-08-854-811-43	Sequence 43, Appl
43	120.4	23.3	891	1	US-08-284-784-33	Sequence 33, Appl
44	120.4	23.3	891	1	US-08-284-784-34	Sequence 34, Appl
45	120.4	23.3	891	2	US-08-854-811-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-142-583A-3

; Sequence 3, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPINK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

```

;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/142,583A
;           FILING DATE: 29-Oct-1998
;           CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: WO PCT/GB97/00658
;           FILING DATE: 11-MAR-1997
;           APPLICATION NUMBER: GB 9605124.8
;           FILING DATE: 11-MAR-1996
;   ATTORNEY/AGENT INFORMATION:
;           NAME: SADOFF, B. J.
;           REGISTRATION NUMBER: 36663
;           REFERENCE/DOCKET NUMBER: 117-263
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 7038164000
;           TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;           LENGTH: 553 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: both
;           TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;           NAME/KEY: CDS
;           LOCATION: 1..363
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

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Query Match          90.4%;  Score 467.4;  DB 3;  Length 553;
Best Local Similarity 96.2%;  Pred. No. 1.2e-134;
Matches 501;  Conservative 0;  Mismatches 16;  Indels 4;  Gaps 2;

```

```

Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db      91 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        ||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
        |||
Db     271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
        |||

```

Db 331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390
 Qy 358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
 ||||||| ||||||||||||||||||||||||||||||||||||
 Db 391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450
 Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
 ||||||| ||||||||||||||||||||||||||||||||||||
 Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510
 Qy 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
 ||||||| ||||||||||||||||||||
 Db 511 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 551

RESULT 2

US-09-142-583A-5

; Sequence 5, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/142,583A

; FILING DATE: 29-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB97/00658

; FILING DATE: 11-MAR-1997

; APPLICATION NUMBER: GB 9605124.8

; FILING DATE: 11-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B. J.

; REGISTRATION NUMBER: 36663

; REFERENCE/DOCKET NUMBER: 117-263

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 341..397
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5
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Query Match          90.4%; Score 467.4; DB 3; Length 553;
Best Local Similarity 96.2%; Pred. No. 1.2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db      91 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          ||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
          |||
Db     271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
          |||
Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
          |||
Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy     417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
          |||
Db     451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy     477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          |||
Db     511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 551
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RESULT 3

US-09-142-583A-10

; Sequence 10, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

```

;      ADDRESSEE: NIXON & VANDERHYE P.C.
;      STREET: 1100 NORTH GLEBE ROAD
;      CITY: ARLINGTON
;      STATE: VA
;      COUNTRY: USA
;      ZIP: 22201
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/142,583A
;      FILING DATE: 29-Oct-1998
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/GB97/00658
;      FILING DATE: 11-MAR-1997
;      APPLICATION NUMBER: GB 9605124.8
;      FILING DATE: 11-MAR-1996
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: SADOFF, B. J.
;      REGISTRATION NUMBER: 36663
;      REFERENCE/DOCKET NUMBER: 117-263
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 7038164000
;      TELEFAX: 7038164100
;
;      INFORMATION FOR SEQ ID NO: 10:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 777 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: both
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: cDNA
;
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 26..493
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

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Query Match          66.3%;  Score 342.6;  DB 3;  Length 777;
Best Local Similarity 87.1%;  Pred. No. 4.4e-96;
Matches 454;  Conservative 0;  Mismatches 14;  Indels 53;  Gaps 5;

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Qy      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy      61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      239 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

```

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      359 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 418
Qy      241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
      ||||||||||||||||
Db      419 ATGCCCCAAGACCCAG----- 433
Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      434 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 489
Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
      ||||||| ||||||||| ||||||||| ||| ||||||||| |||||||
Db      490 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 549
Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
      ||||| ||||||||| ||||| ||||| ||| ||||||||| |||||||
Db      550 TGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 609
Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
      ||||| ||| ||||||||||||||||||||||||||||
Db      610 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 650

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RESULT 4

5405942-2

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,

; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:2:

; LENGTH: 622

5405942-2

Query Match 65.6%; Score 339.4; DB 6; Length 622;

Best Local Similarity 69.7%; Pred. No. 3.9e-95;

Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||||||||||||:|:|||||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      45 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 104
Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
      |||||:~::~:~::~:|||||||||||||||:|:|:|:|:|:|:|:|:|:|:|
Db      105 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCAGCAGUCGGAGGGCGCCUCAG 164
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
      ||||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      165 ACAGGUAUCGUGGAUGAGUGCGUCUCCGGAGCUGUGAUCAUAGGAGGCUGGAGAUGUAU 224

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Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 284
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |:|||||:|||||
 Db 285 AUGCCCAAGACCCAG----- 299
 Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||:||||:||||| ||||:|||||:|||||:|||||:|||||:|||||
 Db 300 ----AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUACAG 355
 Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
 ||:|:| |||||: |:|||||:||||| |||| |||||:||||:||||:|
 Db 356 GAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUUGCUC 415
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
 :|||| |:|:|:| |:| |:| | | |||||:||||:|:| |:|:|
 Db 416 UGCACGAGUUACUGUUAACUUUGAACACCUACCAAAAAUAAGUUUGAUAAACAUUUA 475
 Qy 478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
 ||||: || |:|:|||||:||||:|||||:|||||:|||||
 Db 476 AAAGAUGGGCGUUUCCCCCAUGAAAUACACAAGUAAACAU 516

RESULT 5

US-08-472-809B-8

; Sequence 8, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; TITLE OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,809B
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/209,846

```

; FILING DATE: March 9, 1994
; APPLICATION NUMBER: 07/789,919
; FILING DATE: No. 5925564ember 6, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 214/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5707 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-472-809B-8

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Query Match          55.4%; Score 286.4; DB 2; Length 5707;
Best Local Similarity 85.6%; Pred. No. 2.3e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      853 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
      ||||||||||||||||
Db      1033 ATGCCCAAGACCCAG----- 1047

Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      1048 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 1103

Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
      ||||| |||||||| |||||||||||| |||| |||||||||||| || ||
Db      1104 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGC 1163

Qy      420 TGCA 423
      ||||
Db      1164 TGCA 1167

```

RESULT 6
 US-08-472-809B-7
 ; Sequence 7, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; TITLE OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,809B
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/209,846
 ; FILING DATE: March 9, 1994
 ; APPLICATION NUMBER: 07/789,919
 ; FILING DATE: No. 5925564ember 6, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 214/212
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6345 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-472-809B-7

Query Match 55.4%; Score 286.4; DB 2; Length 6345;
 Best Local Similarity 85.6%; Pred. No. 2.4e-78;
 Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

QY 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||

```

Db      3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761
Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3762 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881
Qy      181 TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3882 TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 3941
Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACGAAGTCTCAGAGA 300
        ||||||||||||||
Db      3942 ATGCCCAAGACCCAG----- 3956
Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
        ||||||||||||||||| ||||||||||||||||||||||||||||||
Db      3957 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 4012
Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
        ||||| ||||||||| ||||||||||||| ||| ||||||||||| || | |
Db      4013 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGC 4072
Qy      420 TGCA 423
        ||||
Db      4073 TGCA 4076

```

RESULT 7

5405942-13

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,

; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:13:

; LENGTH: 357

5405942-13

Query Match 49.4%; Score 255.2; DB 6; Length 357;

Best Local Similarity 98.8%; Pred. No. 2.8e-69;

Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

```

```

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db      103 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db      163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        |||
Db      223 TGCGCACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACCCAGAAGTA 260
        |||
Db      283 ATGCCCAAGACCCAGAAGGA 302

```

RESULT 8

5405942-9

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,

;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:9:

; LENGTH: 357

5405942-9

Query Match 49.1%; Score 253.6; DB 6; Length 357;

Best Local Similarity 79.2%; Pred. No. 8.8e-69;

Matches 206; Conservative 50; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      43 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db      103 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db      163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        |||
Db      223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACCCAGAAGTA 260
        |||

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Db 283 AUGCCCAAGACCCAGAAGGA 302

RESULT 9

5405942-7

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:7:

; LENGTH: 210

5405942-7

Query Match 40.3%; Score 208.4; DB 6; Length 210;

Best Local Similarity 77.6%; Pred. No. 6e-55;

Matches 163; Conservative 46; Mismatches 1; Indels 0; Gaps 0;

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Db      1 GGACCGGAGACGCUCUGCGGGGCUAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy     61 AGGGGCTTTTATTTCACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db     61 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
          :|||||:|||||:|||||:|||||:
Db    181 UGCGCACCCCUCAAGCCUGCCAAGUCAGCU 210
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RESULT 10

5405942-11

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:11:

; LENGTH: 210
5405942-11

Query Match 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 99.5%; Pred. No. 6e-55;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db    121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
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Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
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RESULT 11

US-09-255-829-13

; Sequence 13, Application US/09255829

; Patent No. 6461617

; GENERAL INFORMATION:

; APPLICANT: Shone, Clifford Charles

; APPLICANT: Quinn, Conrad Padraig

; APPLICANT: Foster, Keith Alan

; TITLE OF INVENTION: Recombinant Toxin Fragments

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/255,829

; FILING DATE: 23-FEB-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/02273

; FILING DATE: 22-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/782,893

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

```

;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0130002
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;      INFORMATION FOR SEQ ID NO:  13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  2862 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  DNA (genomic)
;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2862
US-09-255-829-13

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Query Match          40.3%;  Score 208.4;  DB 4;  Length 2862;
Best Local Similarity 99.5%;  Pred. No. 1.9e-54;
Matches 209;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2704 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 2763

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
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Db      2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 2853

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RESULT 12

5405942-15

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:15:

; LENGTH: 210

5405942-15

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Query Match          40.0%;  Score 206.8;  DB 6;  Length 210;

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Best Local Similarity 77.1%; Pred. No. 1.9e-54;
Matches 162; Conservative 46; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 GGACCGGAGACGCUCUGCGGGGCGAGCUGGUGGAUGCUCUUCAGUUCGUGUGGAGAC 60

Qy     61 AGGGGCTTTTATTTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 AGGGGCUUUUAUUUCAACAAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCCTGCCGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    121 ACAGGUAUUCGUGGAUGAGUGCGCUCCGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
        :|||||:|||||:|||||:|||||:|||||:
Db    181 UGCGCACCCUCAGGCCUGCCAAGUCAGCU 210

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RESULT 13

US-08-308-196A-1

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; Sequence 1, Application US/08308196A
; Patent No. 5612198
; GENERAL INFORMATION:
;   APPLICANT: Brierley, Russell A.
;   APPLICANT: Davis, Geneva R.
;   APPLICANT: Holtz, Gregory C.
;   APPLICANT: Gleeson, Martin A.
;   APPLICANT: Howard, Bradley D.
;   TITLE OF INVENTION: Production of Insulin-Like Growth
;   TITLE OF INVENTION: Factor-1 in Methylophilic Yeast Cells
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Brown, Martin, Haller & McClain
;     STREET: 1660 Union Street
;     CITY: San Diego
;     STATE: California
;     COUNTRY: USA
;     ZIP: 92101-2926
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/308,196A
;     FILING DATE: 09-SEPT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/983,523
;     FILING DATE: 03-MAR-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/578,728
;     FILING DATE: 04-SEP-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Seidman, Stephanie L.
;     REGISTRATION NUMBER: 33,779

```

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; REFERENCE/DOCKET NUMBER: 51875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
US-08-308-196A-1
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Query Match          39.2%; Score 202.8; DB 1; Length 240;
Best Local Similarity 96.7%; Pred. No. 3.4e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db      77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db      137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 214
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Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
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RESULT 14

PCT-US91-06452-1

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; Sequence 1, Application PC/TUS9106452
; GENERAL INFORMATION:
; APPLICANT: Brierley, Russell A.
; APPLICANT: Davis, Geneva R.
; APPLICANT: Holtz, Gregory C.
; APPLICANT: Gleeson, Martin A.
; APPLICANT: Bradley, D. H.
; TITLE OF INVENTION: Production of Insulin-Like Growth
; TITLE OF INVENTION: Factor-1 in Methylophilic Yeast Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06452
; FILING DATE: 19910409
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/578,728
; FILING DATE: 04-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51874
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
PCT-US91-06452-1

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Query Match          39.2%; Score 202.8; DB 5; Length 240;
Best Local Similarity 96.7%; Pred. No. 3.4e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        |||
Db      77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136
        |||

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        |||
Db      137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196
        |||

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 214
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Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230

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RESULT 15

US-09-029-267-13

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; Sequence 13, Application US/09029267
; Patent No. 6107057
; GENERAL INFORMATION:
; APPLICANT: Crawford, Kenneth

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; APPLICANT: Zaror, Isabel
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: Pichia Secretory Leader for Protein
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: United States
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,267
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 1165.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

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Query Match          39.2%; Score 202.8; DB 3; Length 390;
Best Local Similarity 96.7%; Pred. No. 4.2e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Db    220 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 279
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
      |||
Db    280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339
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Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 214
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Db    340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373

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Job time : 49.8037 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 230.833 Seconds
(without alignments)
7443.919 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacaat 517

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Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				
Result	Query					
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1	517	100.0	517	9	US-09-852-261-1	Sequence 1, Appli
2	467.4	90.4	523	9	US-09-852-261-5	Sequence 5, Appli
3	377.2	73.0	471	9	US-09-852-261-13	Sequence 13, Appl
4	344.2	66.6	7260	10	US-09-919-497-24	Sequence 24, Appl
5	344.2	66.6	7260	10	US-09-880-107-3739	Sequence 3739, Ap
6	344.2	66.6	7260	13	US-09-873-319-707	Sequence 707, App
7	344.2	66.6	7260	13	US-09-960-706-1066	Sequence 1066, Ap
8	344.2	66.6	7260	15	US-10-136-639-4	Sequence 4, Appli
9	342.6	66.3	725	15	US-10-207-655-54	Sequence 54, Appl
10	325.2	62.9	539	9	US-09-852-261-3	Sequence 3, Appli
11	318.2	61.5	651	15	US-10-161-088-1	Sequence 1, Appli
12	285.4	55.2	612	13	US-10-251-661-7	Sequence 7, Appli
13	258.4	50.0	318	9	US-09-852-261-9	Sequence 9, Appli
14	247.8	47.9	487	9	US-09-852-261-11	Sequence 11, Appl
15	228	44.1	462	15	US-10-238-114-1	Sequence 1, Appli
16	210	40.6	210	13	US-09-807-742-18	Sequence 18, Appl
17	208.4	40.3	2862	13	US-10-241-596-13	Sequence 13, Appl
18	204.6	39.6	4532	10	US-09-930-377B-1	Sequence 1, Appli
19	203.6	39.4	210	10	US-09-930-377B-2	Sequence 2, Appli
20	202.8	39.2	390	15	US-10-179-046-13	Sequence 13, Appl
21	202	39.1	286	15	US-10-161-088-3	Sequence 3, Appli
22	183	35.4	516	13	US-10-029-386-5832	Sequence 5832, Ap
23	182	35.2	182	13	US-10-029-386-18231	Sequence 18231, A
24	140.2	27.1	213	15	US-10-076-816-9	Sequence 9, Appli
25	140.2	27.1	213	15	US-10-077-381-9	Sequence 9, Appli
26	123.8	23.9	621	9	US-09-921-398-40	Sequence 40, Appl
27	123.8	23.9	621	15	US-10-280-826-40	Sequence 40, Appl
28	108.6	21.0	480	9	US-09-921-398-38	Sequence 38, Appl
29	108.6	21.0	480	15	US-10-280-826-38	Sequence 38, Appl
30	101.2	19.6	210	13	US-09-807-742-19	Sequence 19, Appl
31	75.4	14.6	411	10	US-09-960-352-2082	Sequence 2082, Ap
32	72.4	14.0	854	10	US-09-954-531-989	Sequence 989, App
33	71.8	13.9	237	15	US-10-136-841-3	Sequence 3, Appli
c 34	70.6	13.7	447	9	US-09-922-217-917	Sequence 917, App
c 35	70.6	13.7	447	10	US-09-833-263-917	Sequence 917, App
c 36	70.6	13.7	447	14	US-10-025-380-917	Sequence 917, App
c 37	70.4	13.6	437	15	US-10-066-543-663	Sequence 663, App
c 38	70.4	13.6	493	15	US-10-066-543-997	Sequence 997, App
c 39	70.4	13.6	518	15	US-10-066-543-1040	Sequence 1040, Ap
c 40	70.4	13.6	536	15	US-10-066-543-428	Sequence 428, App
41	70.4	13.6	543	15	US-10-136-841-1	Sequence 1, Appli
c 42	70.4	13.6	549	15	US-10-066-543-478	Sequence 478, App
c 43	70.4	13.6	574	9	US-09-922-217-918	Sequence 918, App
c 44	70.4	13.6	574	10	US-09-833-263-918	Sequence 918, App
c 45	70.4	13.6	574	14	US-10-025-380-918	Sequence 918, App

ALIGNMENTS

RESULT 1

US-09-852-261-1

; Sequence 1, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

```
; APPLICANT:  TERENGHI, GIORGIO
; TITLE OF INVENTION:  REPAIR OF NERVE DAMAGE
; FILE REFERENCE:  117-351
; CURRENT APPLICATION NUMBER:  US/09/852,261
; CURRENT FILING DATE:  2001-05-10
; PRIOR APPLICATION NUMBER:  GB 0011278.9
; PRIOR FILING DATE:  2000-05-10
; NUMBER OF SEQ ID NOS:  14
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH:  517
;   TYPE:  DNA
;   ORGANISM:  Homo sapiens
US-09-852-261-1
```

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Query Match          100.0%;   Score 517;   DB 9;   Length 517;
Best Local Similarity 100.0%;   Pred. No. 2.4e-160;
Matches 517;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC  60

Qy     61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181  TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241  ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300

Qy    301  AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAAGTACAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAAGTACAG 360

Qy    361  GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GATGTAGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCT 420

Qy    421  GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 480

Qy    481  GATGGCATTTCGCCCAATGAAATACACAAGTAAACAT 517
        ||||||||||||||||||||||||||||||||||||
Db    481  GATGGCATTTCGCCCAATGAAATACACAAGTAAACAT 517
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RESULT 2

US-09-852-261-5
 ; Sequence 5, Application US/09852261
 ; Patent No. US20020083477A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLDSPIK, GEOFFREY
 ; APPLICANT: TERENCE, GIORGIO
 ; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
 ; FILE REFERENCE: 117-351
 ; CURRENT APPLICATION NUMBER: US/09/852,261
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: GB 0011278.9
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 523
 ; TYPE: DNA
 ; ORGANISM: Oryctolagus cuniculus
 US-09-852-261-5

Query Match 90.4%; Score 467.4; DB 9; Length 523;
 Best Local Similarity 96.2%; Pred. No. 6.le-144;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	476
Db	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Qy	477	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	517

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Db 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521

RESULT 3

US-09-852-261-13

; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

Query Match 73.0%; Score 377.2; DB 9; Length 471;
Best Local Similarity 87.8%; Pred. No. 4e-114;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
|
Db 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
|
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
|
Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy 241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
|
Db 241 ATGCCCCAAGACTCAG----- 255

Qy 301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
|
Db 256 ----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy 361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
|
Db 312 GATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 371

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Qy      420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAA 431

Qy      480 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
          ||||||||||||||||||||||||||||||||||||
Db      432 AGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 469

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RESULT 4

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US-09-919-497-24
; Sequence 24, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-24

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Query Match          66.6%; Score 344.2; DB 10; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          ||||||||||||||||
Db      551 ATGCCCCAAGACCCAG----- 565

Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||||||||||||||| ||||||||||||||||
Db      566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

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Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	370
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	371	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240

Qy 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCCGTGTGTGGAGAC 60
 |||||

; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066

Query Match 66.6%; Score 344.2; DB 13; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

```
Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          ||||||||||||||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||||||||||||||| ||||||||||||||||||||||||||||||||
Db     566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          ||||| |||||||| |||||||||||| ||| |||||||||| ||||||||
Db     622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
          ||||| |||||||| |||| ||||| ||| |||||||||||||| |||||
Db     682 TGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 741

Qy     478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          ||||| ||| ||||||||||||||||||||||||||||
Db     742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782
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RESULT 8

US-10-136-639-4

; Sequence 4, Application US/10136639

; Publication No. US20030072761A1

; GENERAL INFORMATION:

; APPLICANT: LeBowitz, Jonathan

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS
THE BLOOD BRAIN

; TITLE OF INVENTION: BARRIER

; FILE REFERENCE: SYM-008

; CURRENT APPLICATION NUMBER: US/10/136,639

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 60/329,650
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-136-639-4

Query Match 66.6%; Score 344.2; DB 15; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          ||||||||||||||||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     566 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy     361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          ||||| ||||||| ||||||| |||| ||||| ||| ||||||| |||||
Db     622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 681

Qy     420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTTC 477
          ||||| ||||||| ||||| ||||| ||| ||||||| |||||
Db     682 TGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTA 741

Qy     478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          ||||| ||| ||||||||||||||||||||||||||||
Db     742 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 782
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RESULT 9
US-10-207-655-54
; Sequence 54, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.

; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-54

Query Match 66.3%; Score 342.6; DB 15; Length 725;
Best Local Similarity 87.1%; Pred. No. 1.4e-102;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||
Db      216 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||
Db      276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
          |||
Db      336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 395

Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          |||
Db      396 ATGCCCAAGACCCAG----- 410

Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||
Db      411 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 466

Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC 419
          |||
Db      467 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTC 526

Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTT 477
          |||
Db      527 TGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTA 586

Qy      478 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
          |||
Db      587 AAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACAT 627
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RESULT 10
US-09-852-261-3
; Sequence 3, Application US/09852261

; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-3

Query Match 62.9%; Score 325.2; DB 9; Length 539;
Best Local Similarity 81.2%; Pred. No. 6.8e-97;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTTCGGAGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
        || | | | ||||| | ||||| ||||| || ||||| ||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
        ||| ||||| || || ||| | ||||| | || | || | ||||| || |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 470
        || | | ||||| ||||| ||||| ||||| || ||||| ||||| |||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    471 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 528
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RESULT 11
 US-10-161-088-1
 ; Sequence 1, Application US/10161088
 ; Publication No. US20030077761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Parrow, Vendela
 ; APPLICANT: Rosengren, Linda
 ; TITLE OF INVENTION: NEW METHODS
 ; FILE REFERENCE: 13425-111001
 ; CURRENT APPLICATION NUMBER: US/10/161,088
 ; CURRENT FILING DATE: 2002-05-31
 ; PRIOR APPLICATION NUMBER: SE 0101934-8
 ; PRIOR FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 651
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (73)...(471)
 US-10-161-088-1

Query Match 61.5%; Score 318.2; DB 15; Length 651;
 Best Local Similarity 81.7%; Pred. No. 1.5e-94;
 Matches 419; Conservative 0; Mismatches 83; Indels 11; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	139	GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG	198
Qy	61	AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	199	AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG	258
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	259	ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	318
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	240
Db	319	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC	378
Qy	241	ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	379	ATGCCCCAAGACTCAGAAGTCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	438
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	439	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	498
Qy	358	CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Db	499	CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG	558

```

Qy      417 CTCTGCACAGTTACCTGTAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 470
      ||      |      ||||| | || ||| |||      || ||||| ||
Db      559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy      471 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 502
      ||||| ||||| ||||| ||||| ||||| |||||
Db      619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651

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US-10-251-661-7

; Publication No. US20030166555A1

; APPLICANT: Alberini, Cristina M.

; TITLE OF INVENTION: Methods and Compositions for Regulating

FILE REFERENCE: 3499.1001-003

; CURRENT FILING DATE: 2002-09-20

; PRIOR FILING DATE: 2000-03-31

; PRIOR FILING DATE: 2001-04-02

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 7

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

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; NAME/KEY: CDS
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;  LOCATION:  (151) ... (564)
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US-10-251-661-7

Query Match 55.2%; Score 285.4; DB 13; Length 612;

Matches 359; Conservative 0; Mismatches 6; Indels 50; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	247	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	306
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	307	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	366
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	367	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	426
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	427	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	486

```

Qy      241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
          |||||
Db      487 ATGCCCCAAGACCCAG----- 501

Qy      301 AGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
          |||||
Db      502 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 557

Qy      361 GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTT 414
          |||||
Db      558 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612

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RESULT 13

US-09-852-261-9

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; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-9

```

```

Query Match          50.0%; Score 258.4; DB 9; Length 318;
Best Local Similarity 99.6%; Pred. No. 6.6e-75;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||||
Db      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
          |||||
Db      61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
          |||||
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
          |||||
Db      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy      241 ATGCCCCAAGACCCAGAAGTA 260
          |||||
Db      241 ATGCCCCAAGACCCAGAAGGA 260

```

US-09-852-261-11

US-09-852-261-11

Matches 391; Conservative 0; Mismatches 77; Indels 57; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	61	AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC	240
Qy	241	ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	241	ATGCCCCAAGACTCAG-----	255
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	256	----AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAG	311
Qy	361	GATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTC	419
Db	312	AATGTAGGAGGAGCCTCCCAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTGCTG	371
Qy	420	TGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCACA	473

